

Application No.: 10/028482

Docket No.: 3445

AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A system for high throughput detection of genotypes comprising
~~a sample preparation method comprising a method for amplifying a plurality of regions of interest using a method comprising long range polymerase chain reaction amplification of a plurality of nucleic acid samples to form a plurality of amplicons wherein the amplicons are 2 to 15 kilobases and a method for pooling aliquots of a plurality of the amplicons into a plurality of pooled samples for hybridization;~~
a sample preparation automation system;
a sample tracking system;
an automated high density probe array loader ~~comprising a robotic arm and a refrigerated unit;~~
a plurality of high density nucleic acid probe arrays wherein each array comprises about 400,000 different sequence probes, wherein each probe is present in a different feature of the array;
a vacuum-assisted wash station; and
a computer system for managing hybridization data and for analyzing hybridization data to determine the genotype of a sample ~~at a plurality of single nucleotide polymorphisms in a region of interest, wherein said hybridization data are obtained by hybridizing a pooled sample to a high density probe array.~~
2. (Previously Presented) The system of claim 1 wherein the sample preparation automation system is a robotic device for handling multiwell plates.
3. (Original) The system of claim 1 wherein the sample tracking system is a bar code system.
4. (Currently Amended) The system of claim 1 wherein the computer system comprises a processor; and a memory being coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform the step of analyzing the

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hybridization data to determine the genotype of a sample at a plurality of single nucleotide positions in a region of interest.

5-16. (Canceled)

17. (Previously Presented) The system of Claim 1 wherein the sample tracking system and the computer system are linked.

18-20. (Canceled)

21. (Previously Presented) The system of claim 1 wherein said probe arrays have feature sizes of about 20 x 24 microns or smaller.

22. (Previously Presented) The system of claim 21 wherein each high density nucleic acid probe array is capable of simultaneous screening of 30 kilobases of sense nucleic acid sequence and 30 kilobases of antisense nucleic acid sequence.

23. (Previously Presented) The system of claim 1 wherein the high density nucleic acid probe arrays are resequencing or variation detection arrays.

24. (Previously Presented) The system of claim 1 wherein the high density nucleic acid probe arrays genotype a plurality of single nucleotide polymorphisms.

25. (Previously Presented) The system of claim 1 wherein a contiguous sequence is tiled on the high density nucleic acid probe arrays.

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26. (Previously Presented) The system of claim 1 wherein the sample tracking system comprises a single or multiple dimensional barcode system.
27. (Previously Presented) The system of claim 1 wherein the sample tracking system comprises an electromagnetic encoding system.
28. (New) The system of claim 1 wherein the sample preparation automation system is capable of long range polymerase chain reaction amplification of a plurality of nucleic acid samples, thereby obtaining amplicons.
29. (New) The system of claim 28 wherein the amplicons obtained after long range polymerase chain reaction amplification are from 3 kilobases to 15 kilobases.
30. (New) The system of claim 28 wherein the sample preparation automation system is capable of reverse transcribing each nucleic acid sample to obtain cDNA prior to long range polymerase chain reaction amplification.
31. (New) The system of claim 1 wherein the automated high density probe array loader further comprises a refrigerated unit.
32. (New) The system of claim 1, wherein each array comprises 400,000 different sequence probes, wherein each probe is present in a different feature of the array.